

FIG. 1A

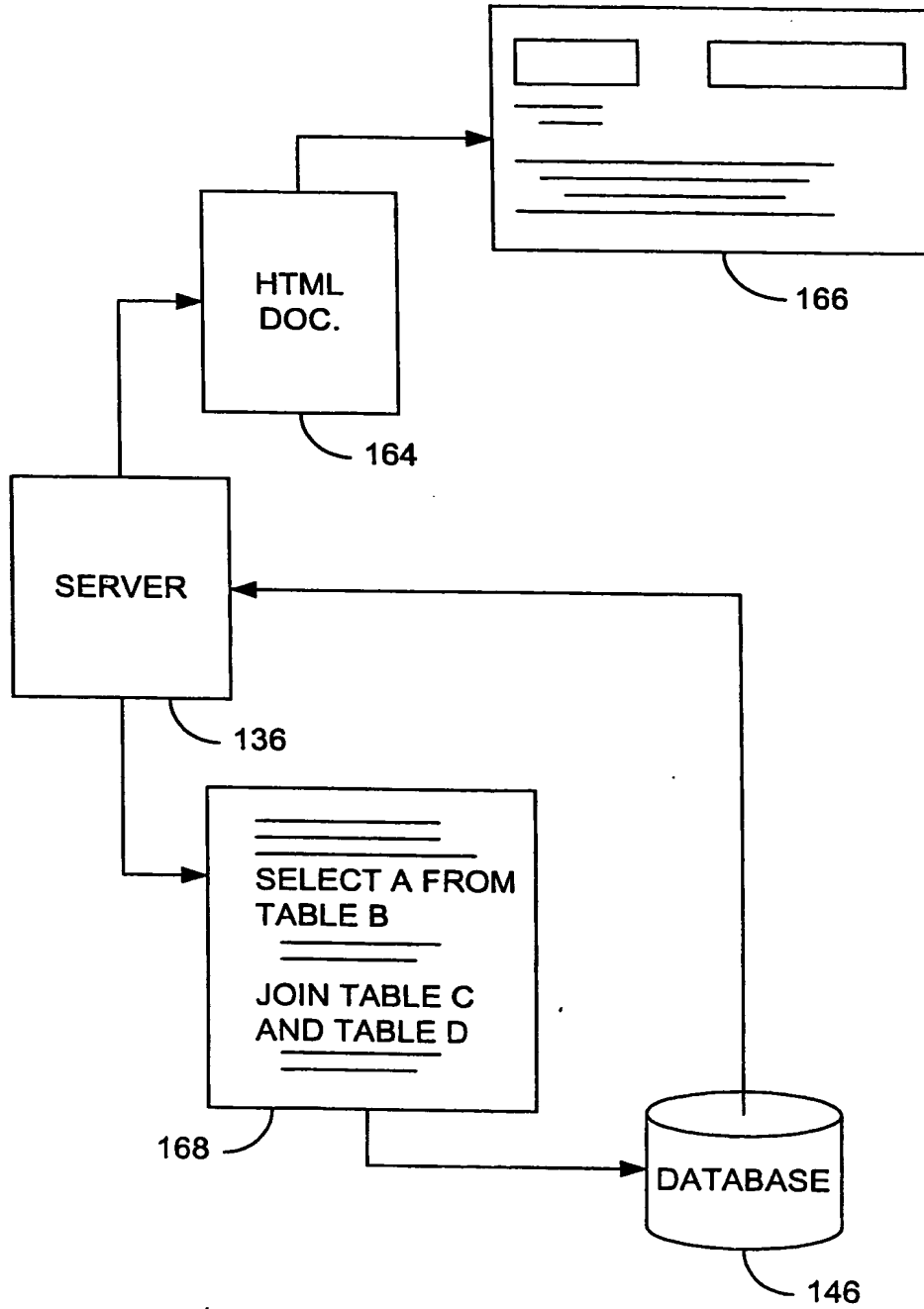


FIG. 1B

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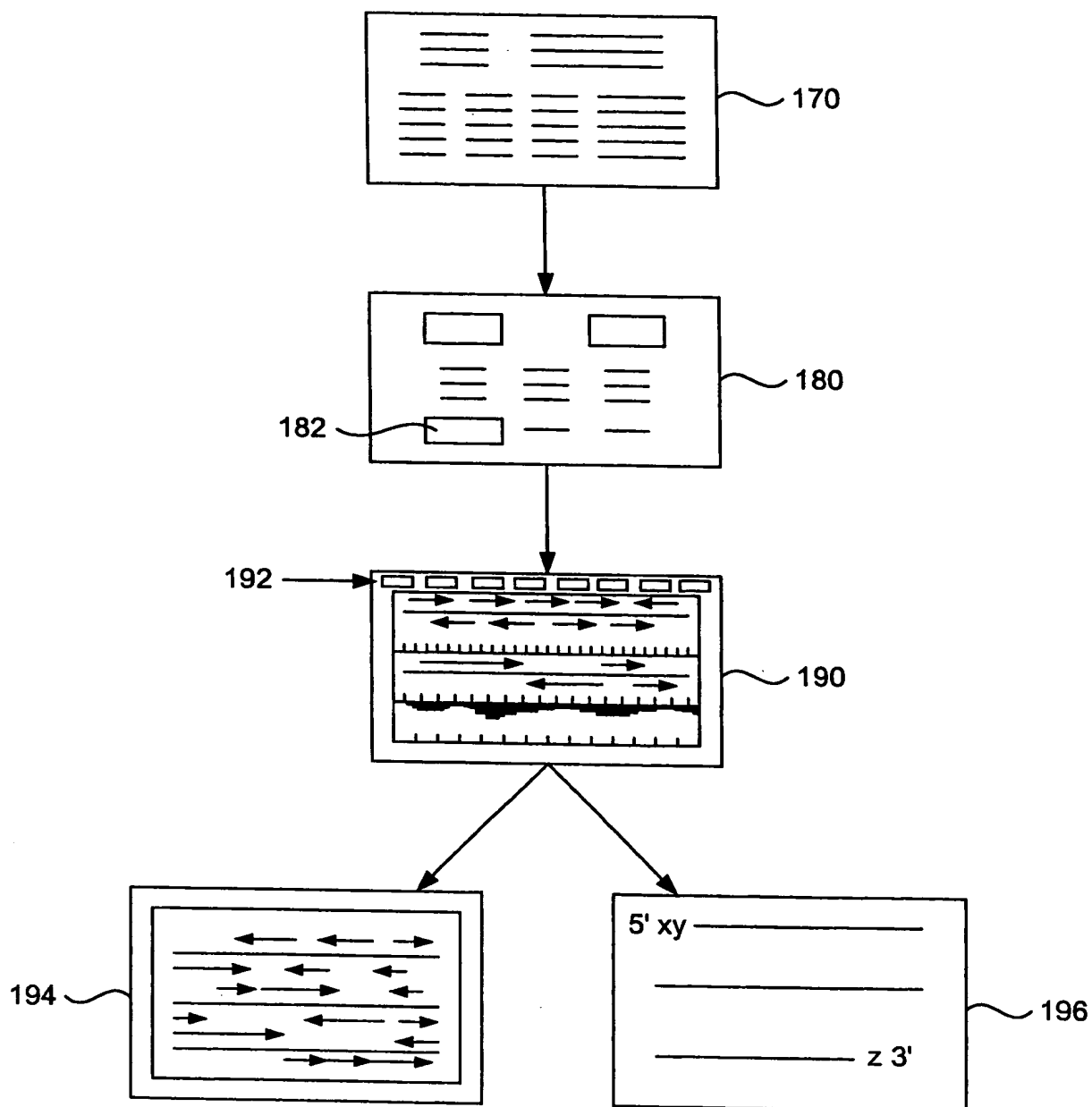


FIG. 1C

Contig Results - Netscape									
Contig Results									
Main Menu	Org Info	Genome	Contig Summary	Contig	Locus Info	Proteins	Comparisons	Southern	Sequences
Library : SAUREU01 Staphylococcus aureus Contigs: 48 Contigs ORFs: 134									
Contig: SAU1c0039 Length: 138277 bp Segs: 1846 Base Pairs Selected: 1 to 138277									
LocusID	Hit ID	Hit Description	Hit Organism	E-Value	Base Pairs	Libs (48)	Seqs		
SAU102730	g2633184	yfh0	Bacillus subtil	3.4e-51	22-2169 (-)	8	26		
SAU103442		LUR		1	2170-2722(+)	0	22		
SAU100689	g2633977	similar to hypothetical proteins	Bacillus subtil	4.8e-62	2723-3559(+)	24	30		
SAU102070	g2633978	ribonuclease H	Bacillus subtil	3.2e-39	3594-4352(+)	34	9		
SAU100241	g2462967	putative succinyl-coA synthetase beta ch	Bacillus subtil	6.8e-123	4467-5621(+)	35	13		
SAU100242	g2633982	succinyl-CoA synthetase (alpha subunit)	Bacillus subtil	2.9e-97	5655-6542(+)	35	10		
SAU102767	g3767593	LytN	Staphylococcus	4.8e-23	6849-6998(+)	3	7		
SAU101151	g3767595	Eph	Staphylococcus	0	7029-8270(+)	13	18		
SAU101152	g2633984	ORF4	Staphylococcus	3.5e-109	8514-9314(+)	36	13		
SAU101153	g2462971	DNA Topoisomerase I	Bacillus subtil	0	9497-11563(+)	48	32		
SAU101154	g2633986	Gid protein	Bacillus subtil	0	11728-13026(+)	43	36		
SAU101155	g2633987	integrase/recombinase	Bacillus subtil	7.1e-51	13440-14333(+)	38	27		
SAU101156	g2633987	beta-type subunit of the 20S proteasome	Bacillus subtil	9.7e-52	14348-14881(+)	21	17		
SAU101157	g2633988	ATP-dependent Cip protease-like	Bacillus subtil	7.4e-95	14971-16350(+)	40	16		
SAU101158	g2633989	transcriptional regulator	Bacillus subtil	1.3e-62	16378-17139(+)	9	8		
SAU100275	g2634021	ribosomal protein S2	Bacillus subtil	2.8e-73	17493-18200(+)	47	12		

FIG. 2

Locus Query - Netscape

*Locus Information*

Search by LocusID: 
 Display: ☒ Locus Details
 ☐  Loci around the selected Locus

~ 302

**Locus ID:** SAU100241      **Type:** Homology      **Gene Category:** Small molecule metabolism  
**C ntig ID:** SAU1c0039      **Position:** 5 of 150  
**Amino Acids:** 385      **Nucleotides:** 1155      **Seqs:** 13  
**Homologs:** 46      **Paralogs:** 1      **Libs:** 35

Top hits: FASTA of ORF against pagenpept110

Hit ID	Hit Description	Hit Organism	E-Value	ORF Coverage
<u>g2462967</u>	putative succinyl-coA synthetase beta ch	Bacillus subtil	<u>6.8e-123</u>	100%
<u>g2633981</u>	succinyl-CoA synthetase (beta subunit)	Bacillus subtil	<u>6.8e-123</u>	100%

FIG. 3

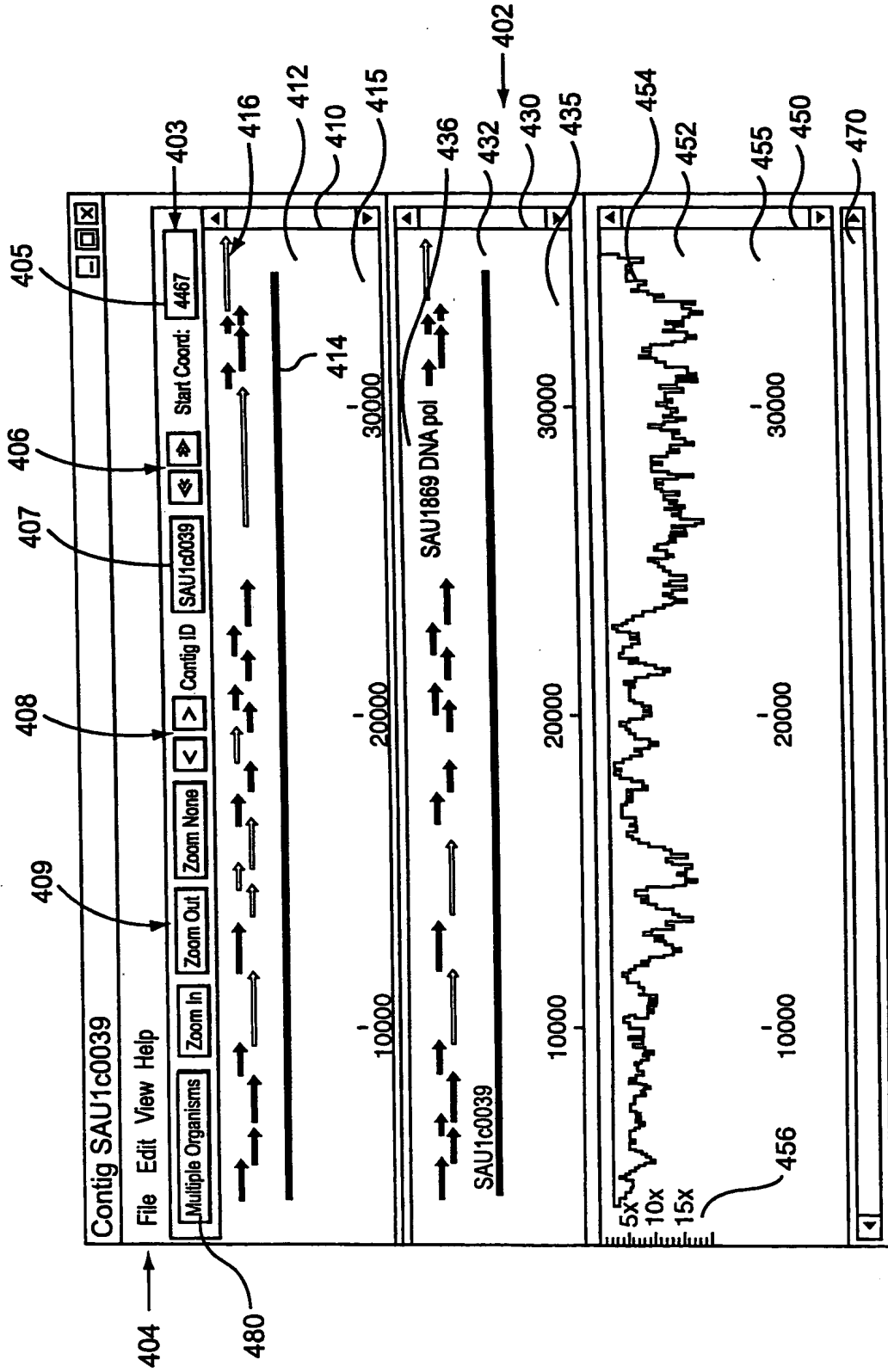


FIG. 4A

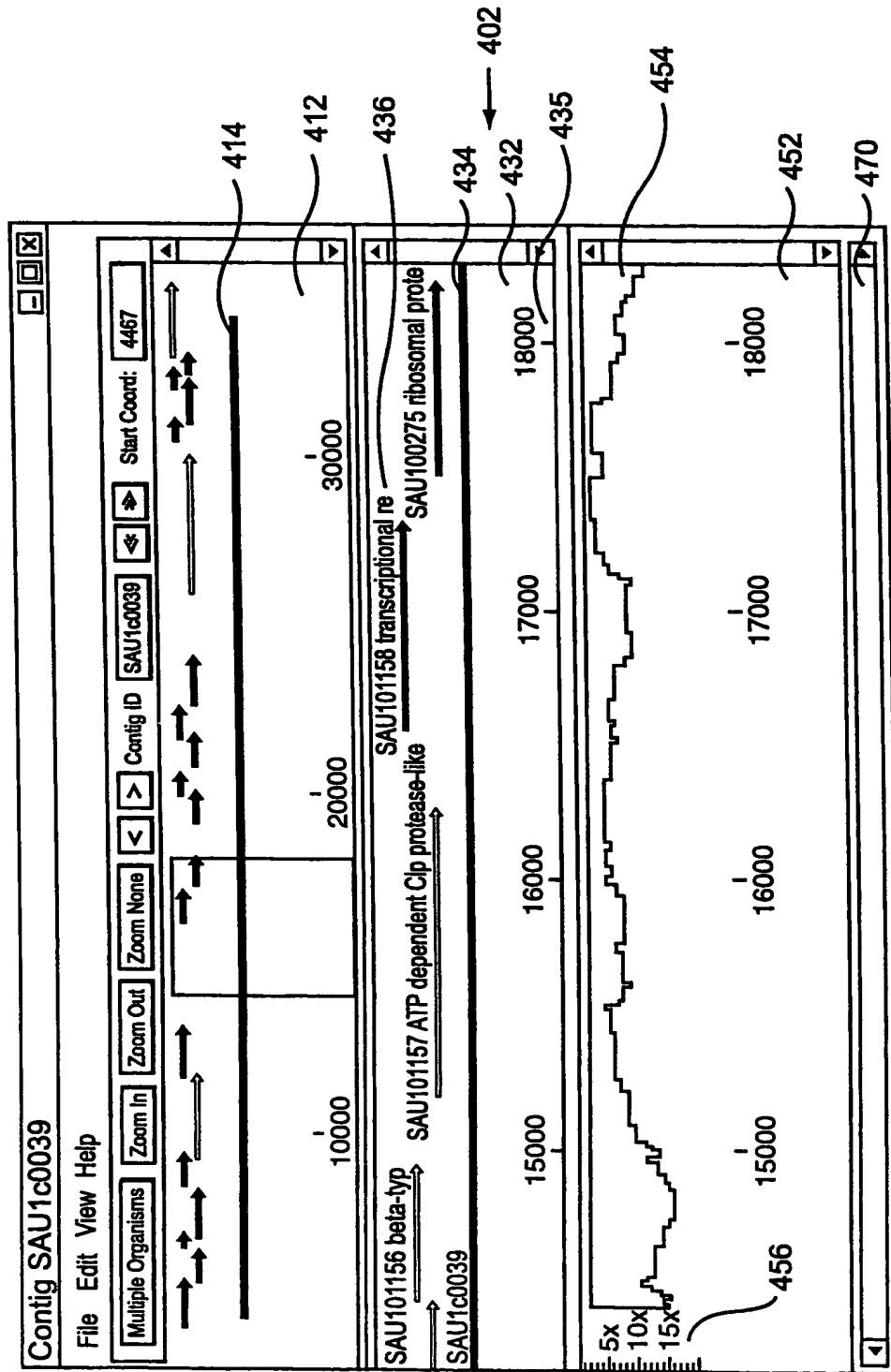


FIG. 4B

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Selected Object Details ✕

Details

Locus ID

Gene Category

Hit Description

EValue

Libs

Seqs

Base Pair

Hit Data Source

Locus Type

HitID1

HitID2

HitID3

HitID4

HitID5

500

502

FIG. 5A



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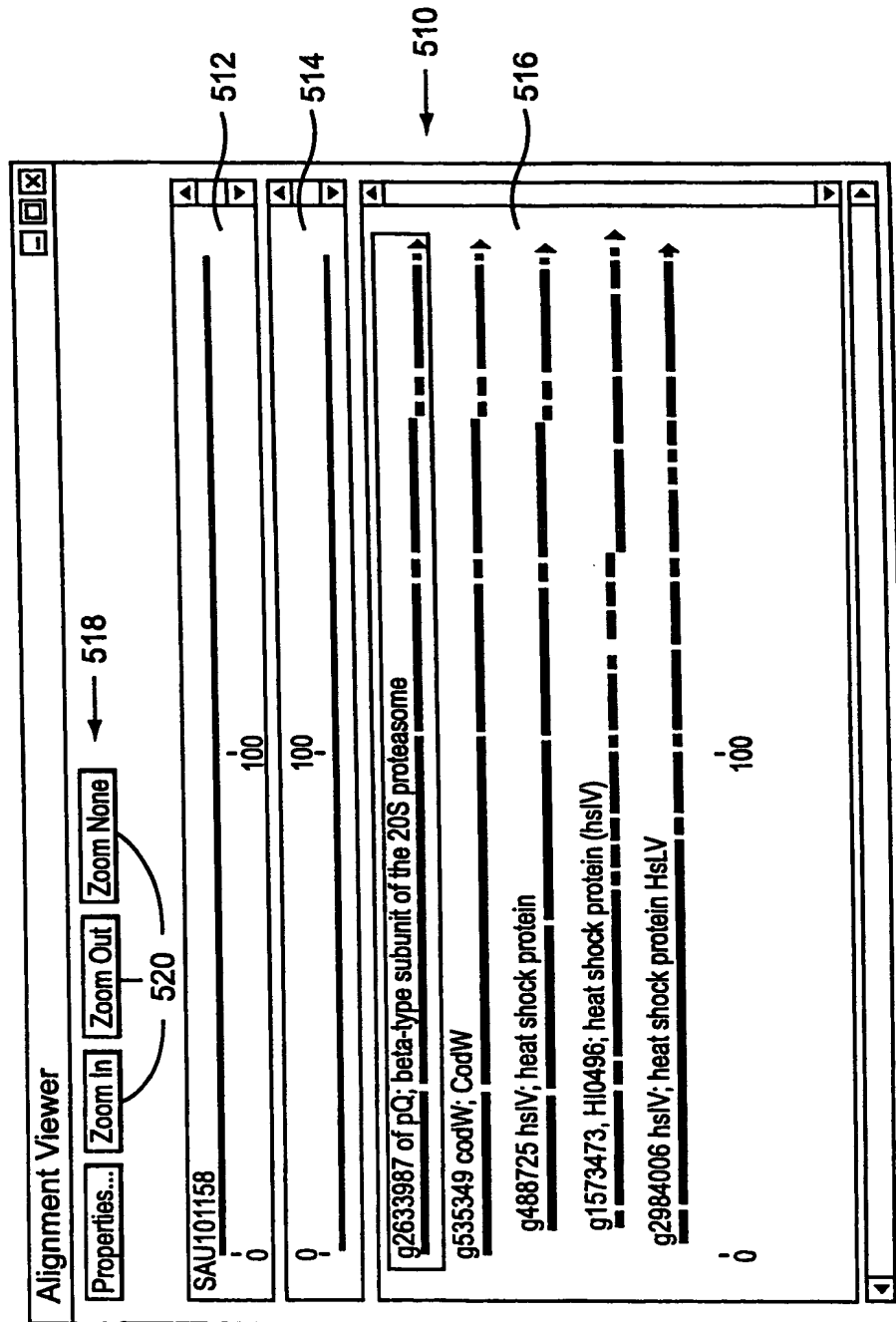


FIG. 5B

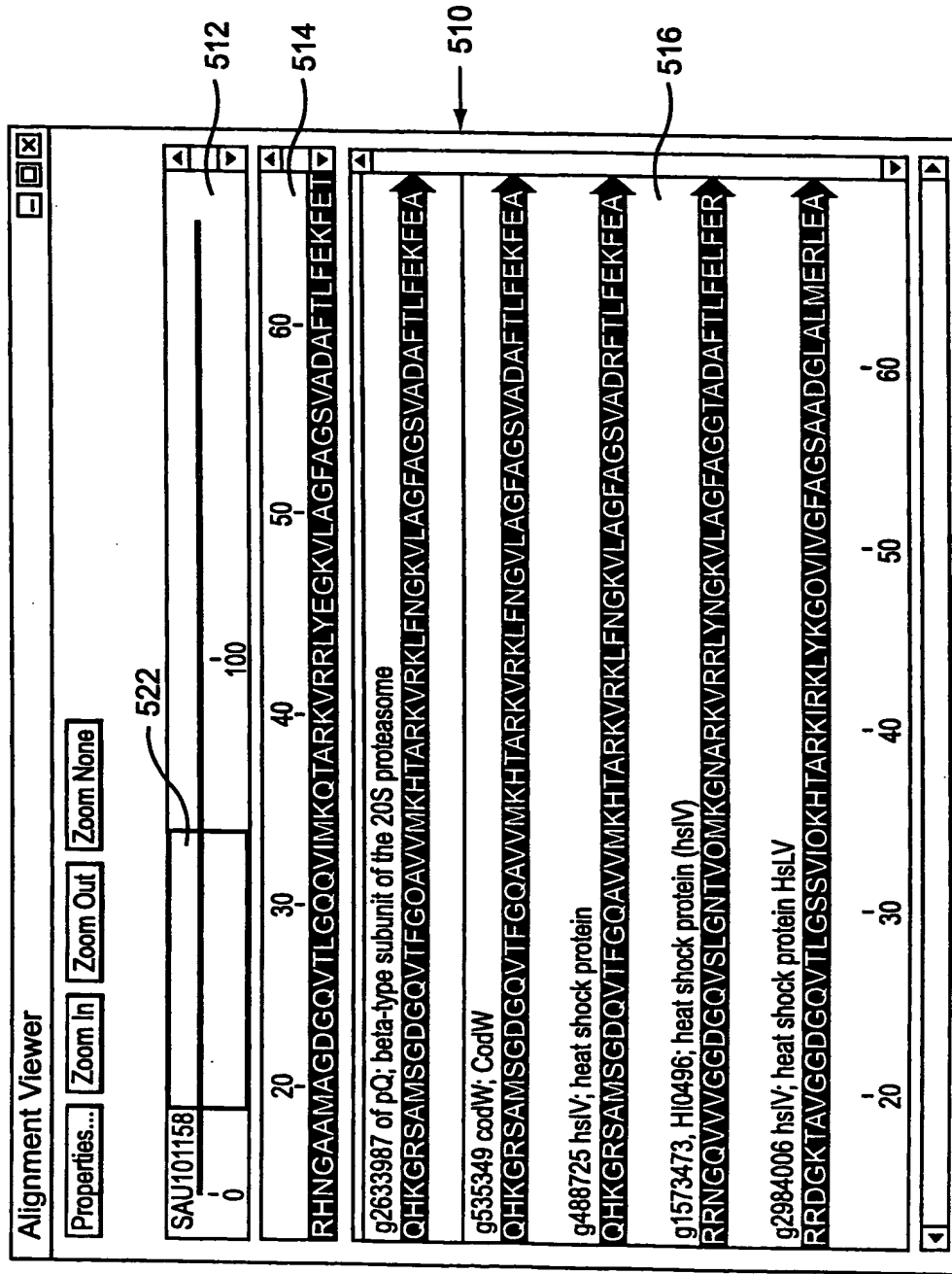


FIG. 5C

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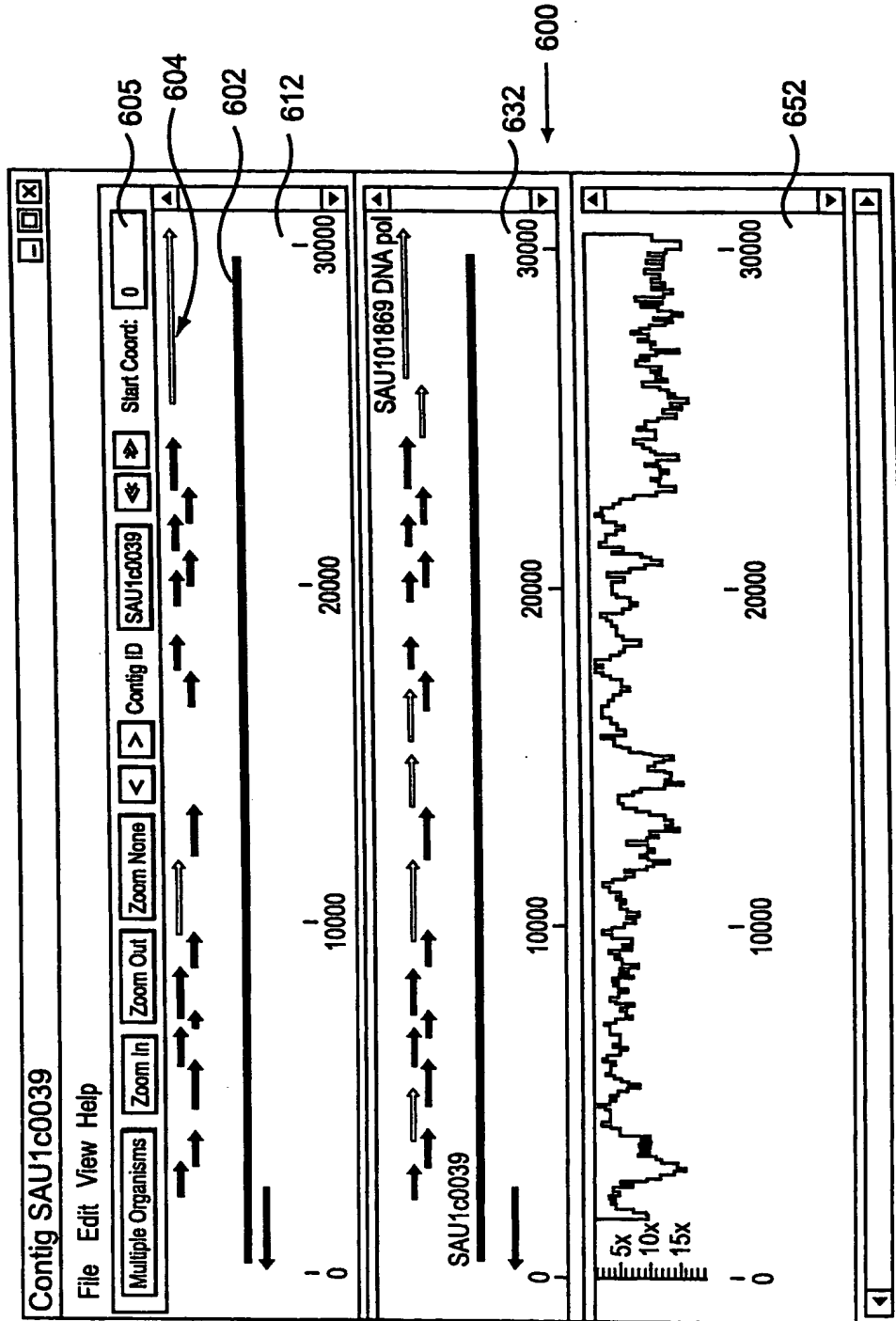


FIG. 6



**FIG. 7**

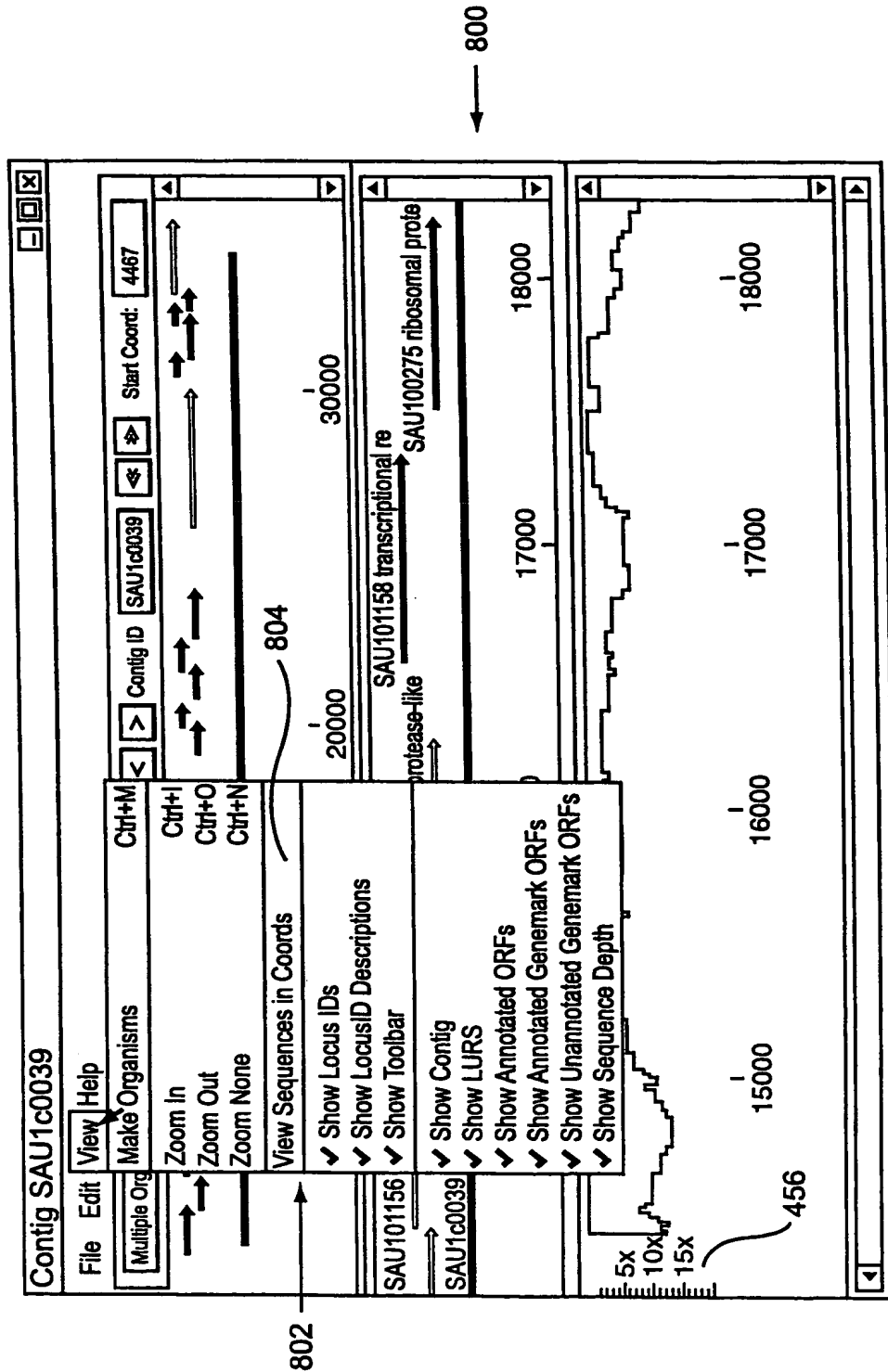


FIG. 8A

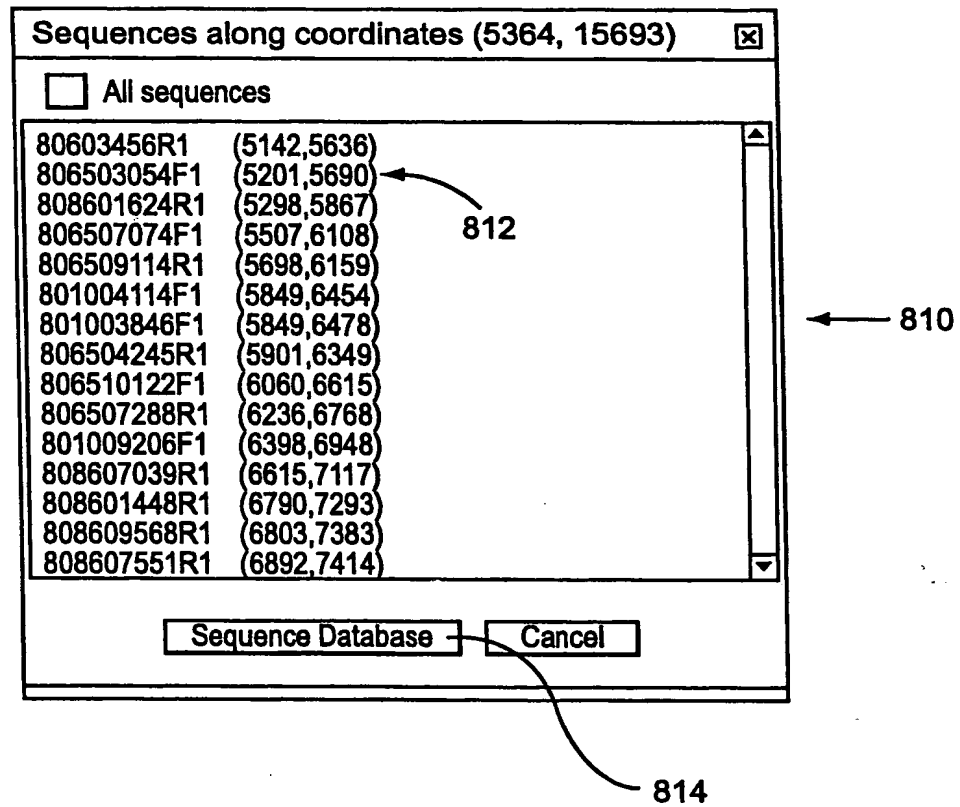


FIG. 8B

Sequence Retrieval Results - Netscape

Sequence Retrieval Results

Main Menu

Org Info

Genome

Contig Summary

Contig

Locus Info

Proteins

Comparisons

Southern

Sequences

Life Tools

Help

Retrieval

BLAST

BLAST2

FASTA

ClustalW

GCG Assembly

Phrap

Translation

Sequence Info

☒ >806503054F1

saureu01

GTCTAAACATGATTATCATACATTGCATTAGATGGTGACATCGGATGTATGGTGAATGGTGCAGGTTTAGCCATGGCAACATGGATACGAATTAATCATTTCGGTGAACCCAGCCAATTTCTAGATCGAGCGGAAGCGCTACTAGAGAAAAAGTAACTGAAGCATTAAATCATTTAGGTGATGAAATGTTAAAGGTATTTTGTAAACATTTTCGGTGGCATTAGAAATGTGATGTTATCGCAGAAGGTATCGTTGAAGCTGTAAAGAAGTAGATTTAACTTTACCACCTAGTTGTACGCTAGAAGGTACAAATGTTGAGTTAGGTAAAAAAATCTTAAAGACTCAGGATTAGCAATTGAACCGAGCAGCAACATGGCTGAAGGTGCACAAAAATTTGTAACTAGTCAAGAAGCATAGGAAGGATGGAGCACTAAGATGAGTGATTATTATAGATAAGAACTAAAGTAAAT

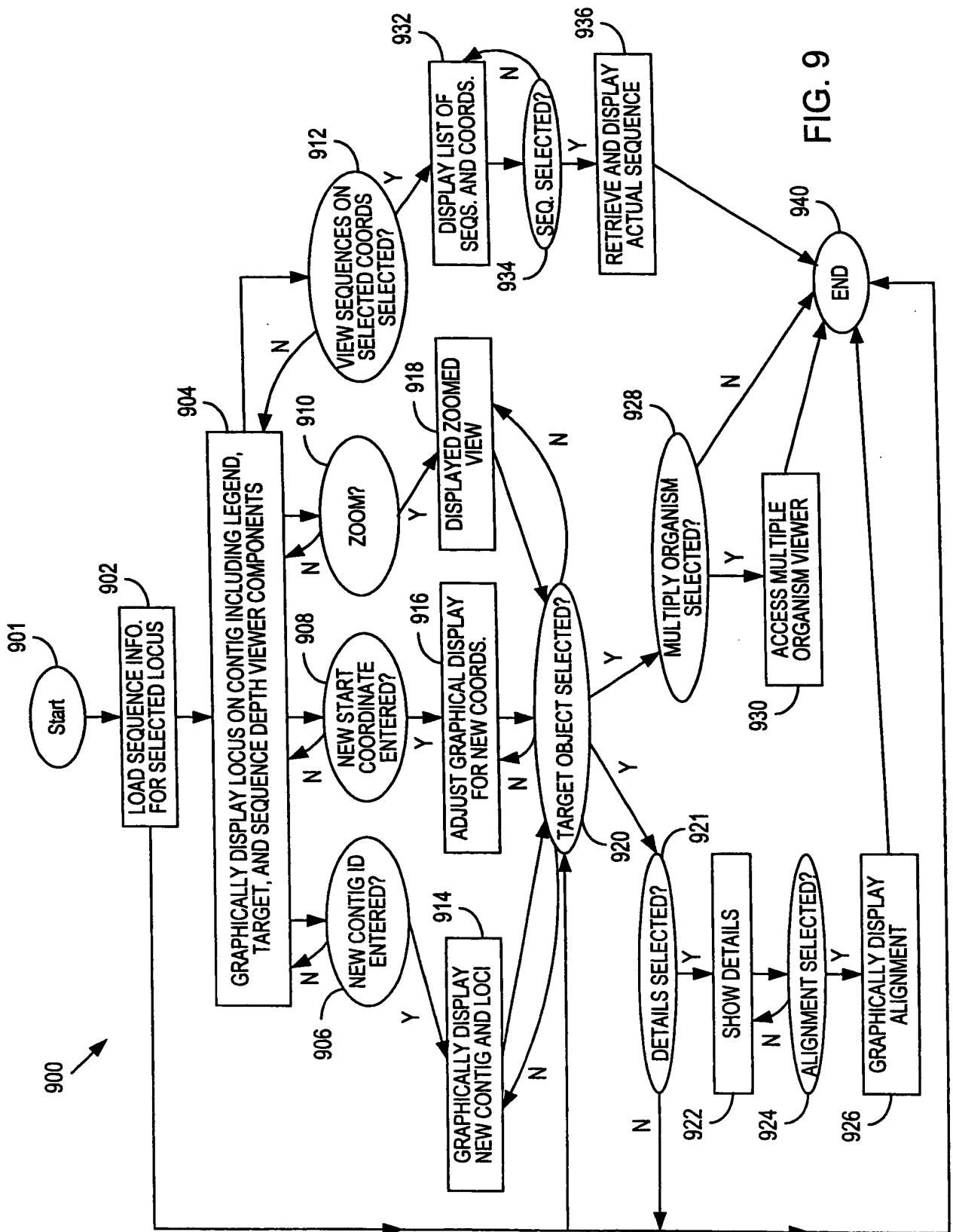
822

Submit sequences to: BLAST

Submit

Reset

FIG. 8C





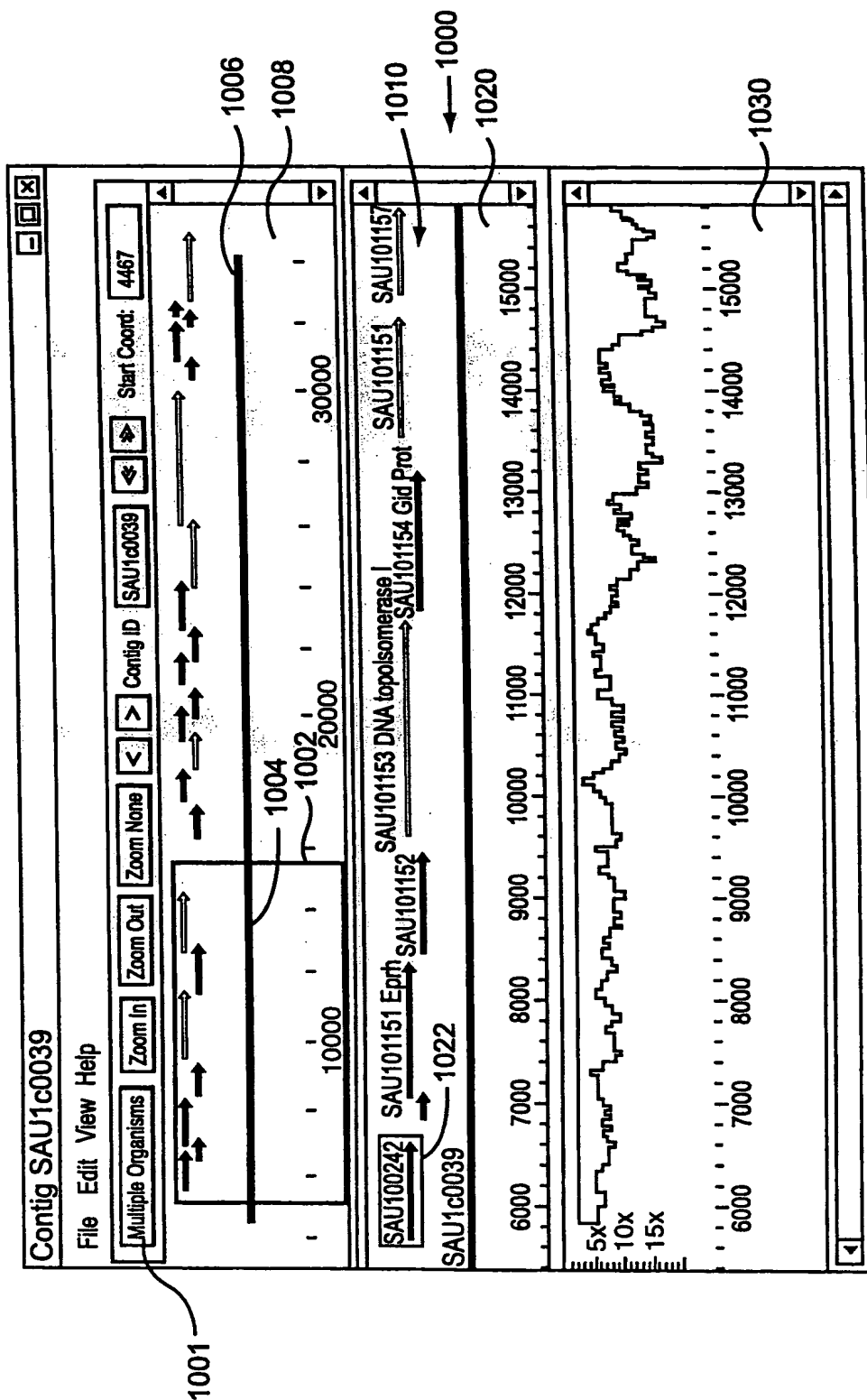


FIG. 10A

Multiple Organism for LocusID - SAU100242 ☒

☐ All Libraries

Paralogs	Library Name
1	SAUREU01 ( <i>Staphylococcus aureus</i> )
2	AAEOLI01 ( <i>Aquifex aeolicus</i> )
2	AFULGI01 ( <i>Archaeoglobus fulgidus</i> )
2	AFUMIG01 ( <i>Aspergillus fumigatus</i> )
1	BFARGI01 ( <i>Bracteroides fragilis</i> )
1	BPERTU01 ( <i>Bordetella pertussis</i> )
1	BSUBTI01 ( <i>Bacillus subtilis</i> )
1	CALBIC01 ( <i>Candida albicans</i> )
1	CJEJUN01 ( <i>Campylobacter jejuni</i> )
1	CPNEUM01 ( <i>Chlamydia pneumoniae</i> )
1	CTRACH01 ( <i>Chlamydia trachomatis</i> )
1	ECLOAC01 ( <i>Enterobacter cloacae</i> )
1	ECOLI01 ( <i>Escherichia coli</i> )
3	FGRAMI01 ( <i>Fusarium graminearum</i> )

← 1040

1042

FIG. 10B

Multiple Organism for LocusID - SAU100242 [X]

☐ Display all Loci

LocusID	Hit Description
SAU100242	succinyl-CoA synthetase (alpha subunit)
CAL07951	probable succinyl-coa ligase
PRT102068	succinyl-CoA synthetase, alpha subunit
SAU200294	succinyl-CoA synthetase (alpha subunit)
SEP100435	succinyl-CoA synthetase (alpha subunit)
SEP100614	ORF1
SHA100180	succinyl-CoA synthetase (alpha subunit)

Multiple Organism — Cancel

← 1045

1046

FIG. 10C

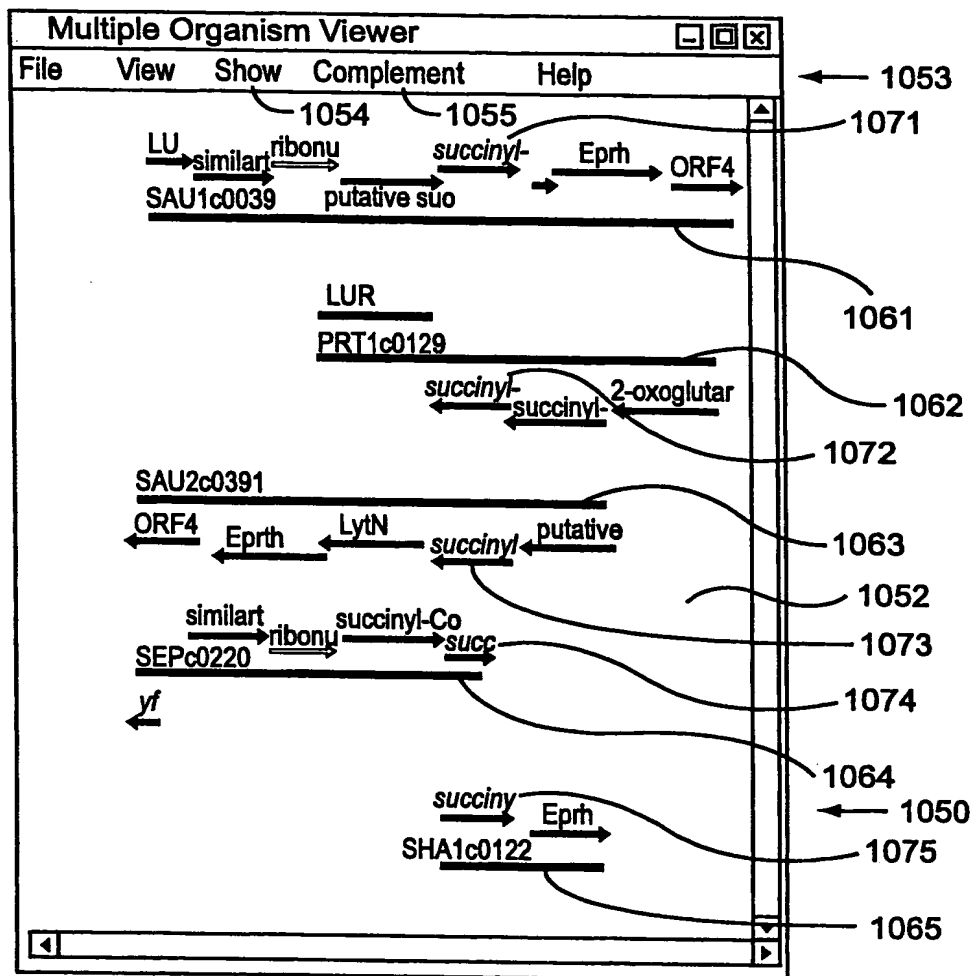


FIG. 10D

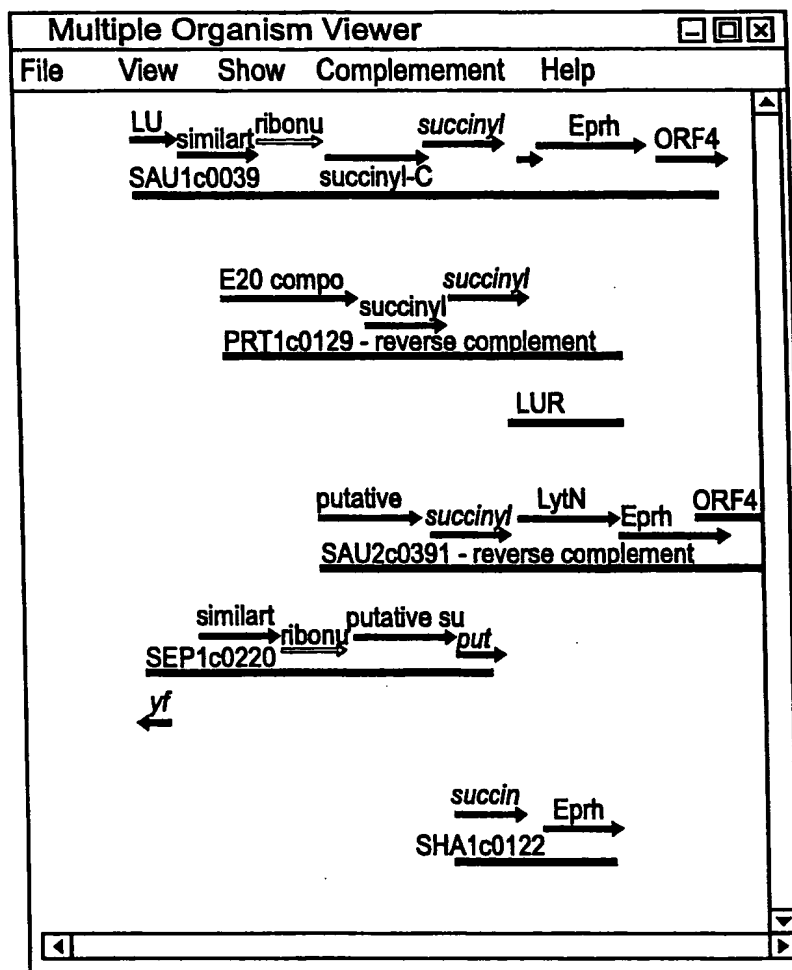


FIG. 10E

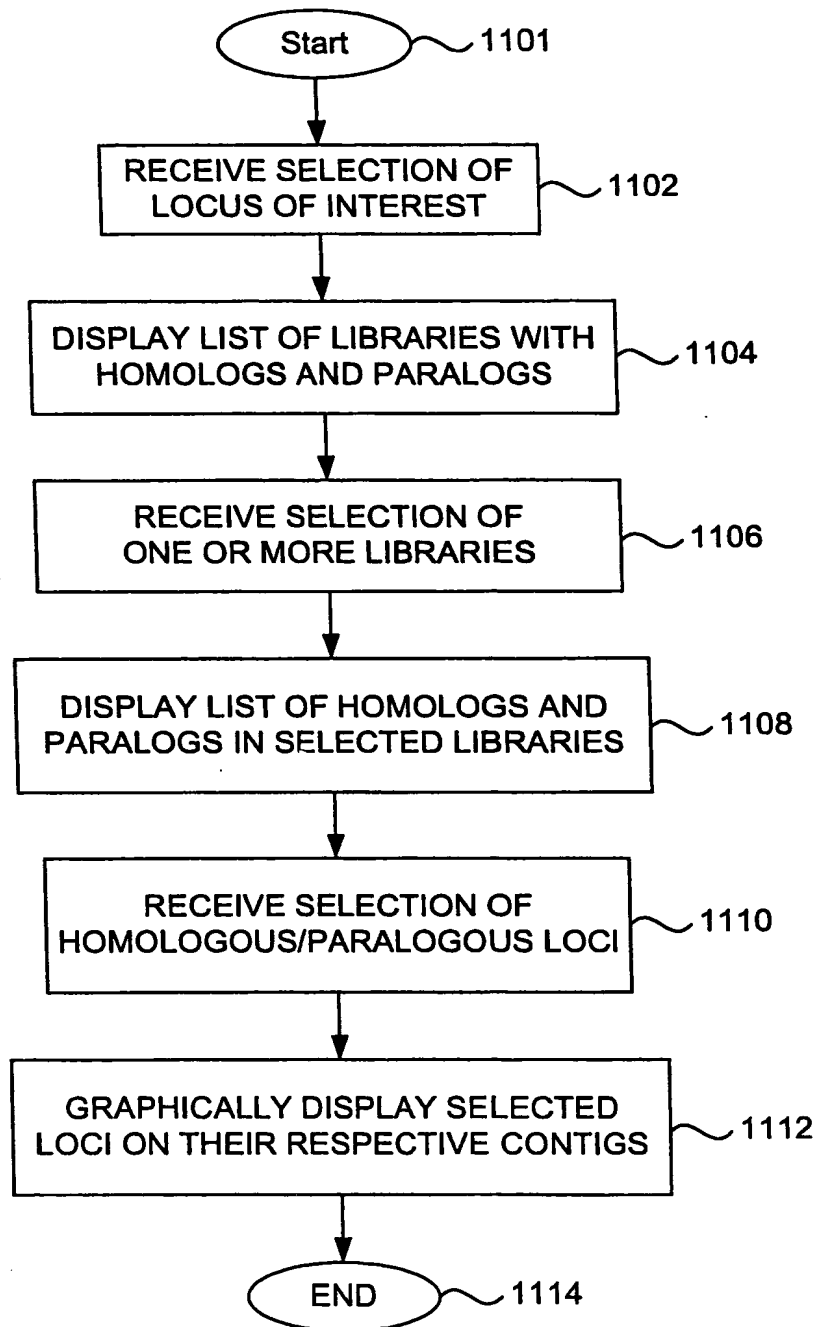


FIG. 11